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ABSTRACT

New simulations for teaching quantitative biological techniques are now used at Michigan Technological University. Traditionally, such techniques work within a particular system and have the student assume certain initial conditions and employ appropriate constants. The computer generates time dependent data which are plotted. The student then repeats the process with changed conditions, observing the changed effect. In the new method, certain initial conditions are established randomly by the computer program and the student generates data to ascertain the unknown quantity, just as if he were measuring on a real system. The procedure is as follows: 1) The computer randomly generates a system parameter which the student must evaluate. The value is stored unrevealed to the student. 2) The computer generates data based upon the unknown constant, student determined input values, and the prepared simulation program. 3) The student uses the data to determine the unknown. 4) Finally, the student compares his derived value with the stored value. This report also provides a detailed simulation example, a procedural flow chart, and a list of other potential training simulation. (PB)

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THE INTRODUCTION OF BIOLOGICAL MENSURATION TECHNIQUES THROUGH SIMULATION

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The use of simulation techniques for presentation of basic biological principles has expanded tremendously over the past several years. In most cases the student is provided with a prepared simulation involving a particular system, for example, predator-prey interaction. The student then assumes certain initial conditions, employs appropriate constants; and the computer generates time dependent data. This data is either plotted out by the computer, or the student plots the data by hand. The student may then repeat the simulation with changed conditions, and observe the effect. By working with the simulation, and by obtaining some understanding of the mathematics involved, the student gains a deeper insight into the basic principles and concepts of biology.

At the 1970 Conference on Computers in the Undergraduate Curricula, held at Iowa City, Iowa, I reported on a variety of biological simulation which could be implemented on the Olivetti microcomputers [1],[2]. Since that time, the list of available programs for this equipment has been extended to include simulations of both the deterministic and stochastic type in practically all fields of biological sciences [3].

During the past academic year, we have employed simulations in a slightly different manner at Michigan Tech with considerable success. Rather than having the student select all the initial conditions for a given simulation, certain initial conditions are established in a random manner by the computer program. The student them employs the program to generate data with the objective of accertaining the unknown quantity, just as he would if he were performing a measurement on a real system. The simulation becomes a teaching aid for training students in the performance of some quantitative technique in biology. The advantage of this approach is that the student is provided with an individualized set of data which he must employ to evaluate one or more system parameters that are unique to his set of data. In terms of quantitative procedures, this training should be just as effective as if he were working with a real system.

The basic technique is as follows:

1. The computer employs a random number routine to generate the particular system parameter which the student is assigned to evaluate. The value is stored for use in the simulation without being revealed to the student.

2. Next, the computer generates a set of data based on the unknown constant, student determined input values, and the prepared simulation program.

3. The student then employs the data to determine the unknown parameter, perhaps using some graphical procedure.

4. Finally the student obtains a printout of the unknown parameter to compare with the value which he has derived from the simulation data.

As an example of a training simulation of this type, consider the following which was developed for use in the ecology course at Michigan Tech, and is designed to introduce the student to the technique of estimating a population by the mark and recapture technique. The simulation has been programmed for the Olivetti P-602 microcomputer. The computer flow chart of the simulation is presented in Figure 1.

Mark and Recapture Simulation

The basic mark and recapture method of estimating populations of organisms involves taking a moderately large sample, marking them in some manner, and returning them to the original group. At some subsequent time, additional samples are withdrawn and inspected to determine the fraction of marked individuals. The basic equation (Peterson) for estimating the population is as follows:

$$p = \frac{S}{r} \cdot M$$

where p is the population estimate, S is the number sampled, r is the number of originally marked organisms which were recaptured, and M is the total number of marked organisms in the population.

This process is simulated using the Monte-Carlo technique by generating a random number to establish the true population size. This random number is then stored in the computer without being printed out. The operator assumes a certain number of originally marked organisms, which he enters into the computer. The sample size is also entered. The computer then sets up a ratio between marked organisms and the total population, and simulates the sampling process by generating a series of random numbers equal to the sample size. Each one is checked against the ratio between marked and total. The computer keeps track of the number of times the random number is greater than that ratio, and records these as unmarked organisms. The ratio is continually modified to reflect the changes in marked and unmarked organisms in the population as a whole. At the end of the "sampling" the computer prints out the number of marked, and unmarked organisms in the sample, the total number of marked organisms in the population, and the population estimate based on three different equations:

Peterson: $p = \frac{m(u+r)}{r}$

Schnabel: $p = \frac{\Sigma m(u+r)}{\Sigma r}$

Schumacher-Eschmeyer: $p = \frac{\Sigma m^2(u+r)}{\Sigma mr}$

where m = the total number of organisms marked.
r = the number of marked organisms in the sample.
u = the number of unmarked organisms in the sample.

At the end of each sampling the unmarked organisms are considered to have been returned to the population as marked organisms.

The operator may have repeated "samplings" to observe the effect on the estimates which he obtains. When he is satisfied that his estimate is correct, he may call for a printout of the actual population.

Figure 2 shows a plot of typical data obtained when 100 individuals were "marked" and then 11 samples of 50 individuals each were simulated by the computer. Note how the population estimates converge on the computer generated population of 1078. The stochastic nature of the simulation demonstrates quite nicely the magnitude of the deviations that one observes in this kind of measurement technique, and illustrates the pedagogic value of the simulation.

Although this approach has been employed for the development of only a few simulation of mensuration techniques, the following list suggests the broad applicability of the method in other areas of biological sciences.

Other Potential Training Simulations in Biology Include:

1. Delury estimate of population size.
2. Michaelis-Menton constant for enzyme kinetics.
3. Inhibition type, inhibition constant for enzymes.
4. Titration curve for amino acids, pka determination.
5. Extracellular fluid space determination.
6. Molecular weight determination from diffusion data.
7. Molecular weight determination from osmotic pressure.
8. Half life and decay constant for radioactive decay.
9. Chemical equilibrium constant determination.
10. Chemical reaction rate constants, reaction orders.

11. Linkage strength and genetic mapping.

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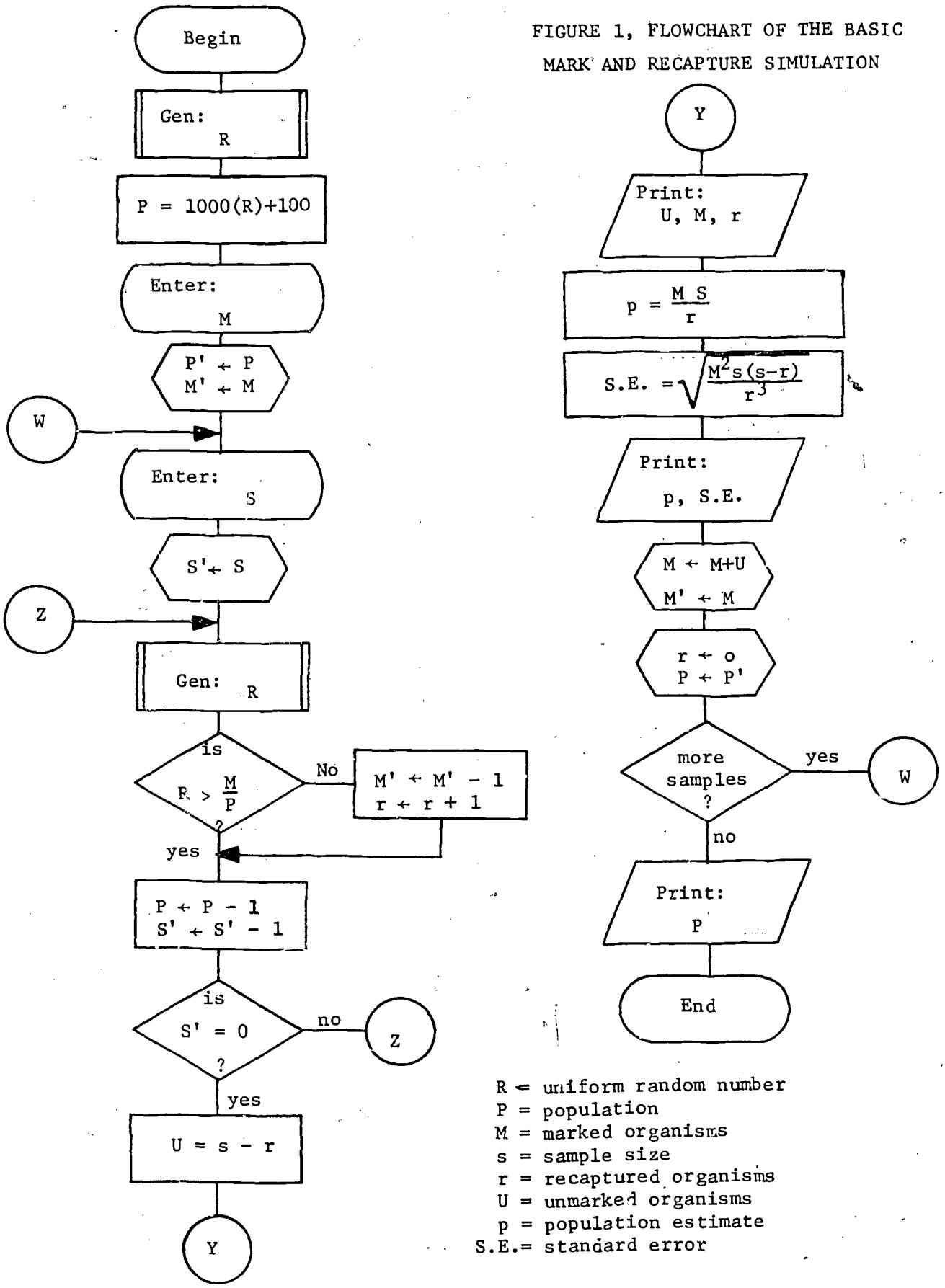

FIGURE 1, FLOWCHART OF THE BASIC MARK AND RECAPTURE SIMULATION

R ← uniform random number
P = population
M = marked organisms
s = sample size
r = recaptured organisms
U = unmarked organisms
p = population estimate
S.E.= standard error

FIGURE 2 - GRAPH OF DATA FROM MARK AND RECAPTURE SIMULATION